those at midline long and slender, the most lateral ones small and peglike. Outer dististyle, *d*, relatively small, about equal in length to the inner style, setae pale; inner style on outer margin of the beak with about 20 long powerful yellow spinoid bristles, the remaining setae shorter, black; face of style in the position of the lower beak bearing a long slender darkened rod, above this with a broad blackened plate that narrows to an acute spine. Aedeagus very long and stout, as in the subgenus.

Holotype male (broken), taken ABOUT 10 ROAD MILES NORTHEAST OF MADERA, CHIHUAHUA, MEXICO, at 7300 feet, 29 September 1966, on flowers of *Lopezia gracilis* (Onagraceae) by D. E. Breedlove.

I am pleased to name this distinct fly for the collector, Dr. Dennis E. Breedlove. Approximately 35 regional species of the subgenus now are known, as discussed in the *Crane flies of California* (Alexander, C. P., Bulletin of the California Insect Survey, volume 8: 56–60, 1967) and in various other papers that concern the species of Mexico. All of these differ from the present fly in hypopygial characters, most evidently in the long powerful bristles on the beak of the inner dististyle, a unique character in this subgenus but occurring in various members of the subgenus *Indotipula* Edwards in the Oriental and eastern Palaearctic regions.

The Nature of Taxonomic Data

RICHARD E. BLACKWELDER
Southern Illinois University, Carbondale

The data of taxonomy is a subject that would scarcely have been discussed even a few decades ago. There was no need to talk about it, because every taxonomist knew what data were relevant in his field, or thought he did, and the only thing to discuss was whether or not he was right—whether there might be a better choice of data in that particular case.

The idea of discussing taxonomic data in general occurred to taxonomists only as a result of the claims and challenges of some non-taxonomists, who thought they had discovered serious faults in the taxonomic system and great failures of taxonomists. These challenges were a surprise to most taxonomists, who were so busy with their endless work that they had never stopped to think about their data in any theoretical sense. Many of them never have understood what all the shouting is about, because they're generally unable to use the supposedly "new" data urged on them by the outsiders, and they've seen only occasional need to do so.

Zoological and also botanical classifications are based entirely on data --data about the attributes of the organisms. This general word attribute is used rather than character to emphasize that "characters" don't have to be structural (what in entomological circles is usually called morphological). To be useful in classification, the data must be comparative in nature—either the organisms agree in possessing the attribute, or they differ in its possession or extent. The differences may be such as to attract our attention through any one of the senses, but most commonly through direct vision. On the other hand, the difference may be such as to appear only after the application of special techniques—microscopy, experimentation, analysis of measurements, chemical analysis, instrumental recording and interpretation of invisible attributes, and so on.

It should be clear that any fact that can be known about an individual or a kind-of-organism is potentially comparative. It can at some future time be compared with the corresponding fact about some other individual or kind. The corresponding features will then be found to be the same or different, to unite or separate the two individuals or groups.

Not *all* comparative data will be taxonomic. At the species level it often will *not* be. Knowledge of the biology of the organisms will enable the taxonomist to eliminate sex-likened differences, pathological differences, differences due to age, developmental stage, caste, and so on. But the *remaining* comparative features are automatically taxonomic. They are the things in which in taxa are alike *or* different.

Not only are all taxonomic data comparative in nature, by definition, but, turning this around, all comparative data *may* be taxonomic, and they must all be studied to determine whether they are variation within the species or diversity among kinds. (By study, is not meant anything very formal; background knowledge usually makes it unnecessary to spend much time on this.)

Taxonomy, especially in entomology, was once almost exclusively "morphological"; it used principally data of structure, especially external structure. For many years taxonomy has been making use also of other kinds of data whenever they are available. In many parts of the Animal Kingdom these newer data have not been needed to any great extent and so have been little used. But taxonomy *can* use *any* comparative data, and *all* comparative data are automatically of taxonomic interest.

The use of comparative data isn't new, even if we now have some sorts of comparative data that weren't available at all a few decades ago. But very few sorts of data available today in any usable quantity are entirely new. Genetic data were used long ago in the form of breeding compatibility. Biochemical data of a rough sort were used more than half a

century ago. X-ray observation and infrared spectroscopy had to await invention of the machines, but they have not yet produced data in sufficient quantity to be really useful in classification.

There are four words basic to this discussion. They are: comparison, resemblance, difference, and correspondence.

Classification implies that there are "classes" of things. If we start with individual things and compare one with another, we can unite similar ones in classes based at first thought on similarities. If we start with many things at once and divide them into classes and subclasses, we will have used differences as our first criterion. These two approaches are the two basic methods of classifying. Both of them are based on comparison of the objects or their attributes. In the first we compare to find what there is that's similar. In the second we compare to find what there is that's different. The key word and concept is comparison.

To group, or classify, things there must also be some similarities among them. This is resemblance. We know that resemblance may be produced by several processes or circumstances (heredity, convergence, or chance), but it's the existence of resemblance that allows comparison to recognize groups, and it's the existence at the same time of differences between organisms that allows us to classify these groups by comparing them among themselves.

Two things can be compared even if they have nothing in common, but there may seem to be no purpose to the comparison. If you had a bottle in which there was a big cerambycid beetle, would you find it useful or even entertaining to compare the bottle with the beetle? It would be pointless, because there's no correspondence of features to make the comparison meaningful. There must be correspondence before we can classify by comparing. There are various ways in which things can correspond: in structure, in shape, in position, in embryological development, in function, and so on. All classification is based on the belief that we can find useful correspondence, what we call homology, in a combination of structure and development and location. We believe that this correspondence is due to the fact that the animals had a common ancestry.

We've been considering taxonomic data so far as if we had already discussed what this expression means. Let's go back now and establish the relationship between taxonomic data (that is, taxonomic features or taxonomic evidence) and the diversity of animals.

The diversity of animals is simply endless. It would be impossible to catalog what we know of it completely because that is even now increasing steadily. We tend to forget the extent of the diversity, because we

can make our distinctions with reference to only a small part of it. The minute we start to talk about the extent of diversity, we get into trouble, because there's no effective way to classify or describe it. For example, we think of the digestive tract as being quite similar in different groups of insects, differing in details of size, shape, and such things, but showing no diversity within a family or genus, and therefore serving as a distinctive character only at high levels. We may assume that this is always true. We forget that there are groups of animals in which the *individuals* in one interconnected colony may differ in possessing a digestive tract or not. Diversity exists at all levels, and there is no theoretical way to tell what level will be exemplified by any particular sort of feature.

What we, as taxonomists, are interested in is that some of the diversity is useful to us and some is not. The part that is not useful can't be forgotten, however, as it must be recognized in order to be avoided. The useful part is what we just called comparative data. When we compare, the similarities allow us to group like things; the differences allow us to separate unlike things. But because taxonomists seldom are interested in grouping or distinguishing individuals, the features must be ones that don't vary within the species (or other group).

That individual variation is not a simple matter, a single sort of diversity, is suggested by this abbreviated list of the causes of diversity within the species:

1) Normal developmental processes
2) Sexuality
3) Colonial division of labor
4) Genetic recombination and ploidy
5) Mutations
6) Response to environment
7) Combinations of these

If your reading takes you outside of the field of entomology (and I hope it does), you may sometime note that G. G. Simpson once wrote that one cannot classify individuals, but only species. There's a sense in which this is true; for example, if all the species are known, as in the higher vertebrates, then one classifies only species and groups of species. In most of the Animal Kingdom, however, we *must* start with individuals and determine which belong to one species and which to another. We would like to do this by knowing enough about them to say that they are the members of an interbreeding population and thus are genetically related. It's extremely rare that we can do this, because a species is not a population but a complex of local populations which we never can actually see.

What the taxonomist does is to assign to one species all the specimens which his comparative studies lead him to believe are related *because* they are as alike as their offspring or their hereditary relatives within a few generations. Many biologists find this definition unsatisfying, but it's the actual basis of most taxonomic work. It has been worded even more simply, that a species consists of whatever individuals the taxonomist thinks belong to it, but this fails to make clear that he thinks this because he *believes* that their similarities are due to the fact that they are genetically related. He puts them together because of the comparative features, but with the assumption that these reflect actual kinship.

There have been several attempts in the past 30 years to change the philosophical or methodological basis of taxonomy. There has been much discussion of these, but it's questionable whether they have had much effect on the practicing taxonomist. The first of these, and the one most bitterly fought over, was the claim that taxonomy is a branch of the study of evolution; that its principal purpose is to unravel the course of evolution; and that its classifications are based on phylogeny. This is The New Systematics as defined by Mayr; Huxley and his collaborators in the original *New Systematics* book did not make this claim.

Nowadays, no biologist denies that animals have undergone changes, that these changes coming in succession have produced new kinds, that this "evolution" has produced all the kinds we now know, and that the history of the kinds is phylogeny, the record of the successive changes.

No entomologist uses phylogeny to a significant extent in his taxonomy because there isn't enough known about the phylogeny of insects. It is curious, however, that we come to think of phylogeny as something more than a theoretical concept. It's quite possible that if we knew the phylogeny of every species, we could classify them on this basis. (It's *more* likely that we'd find it unnecessary or even impossible to classify this way.) But we don't know the phylogeny of even one species. We have merely worked out a scheme, in such a case as the horse, which we think may have been its phylogeny, and which we hope was, to bolster our ego.

Where does this supposedly phylogenetic data come from? There are two sources: First, the sequence of fossils in successive layers of rocks gives a direct clue to succession of these forms in time. But this is highly subjective, and it won't work at all until taxonomic comparisons of the specimens convinces the paleontologist that the successive forms are related.

If you found a bone in a relatively old stratum and a spiral shell in a younger stratum in the same sequence, as you very likely could do, you

wouldn't conclude that the snail evolved from the horse. You'd know that they are unrelated and not comparable.

The second source is direct comparison of the animals, or their fossil remains, in the usually subjective taxonomic manner, to see which one has features that could have been derived from corresponding features of the other. In either case the result is not *the* phylogeny of the animal but a *supposed* phylogeny. If the work has been done well, it may be a very convincing supposed phylogeny.

But, if the phylogenies are based essentially on comparative data, then a classification supposedly based on phylogeny is actually no different in basis from one based *directly* on comparative data. There simply are no real distinct data of phylogeny, although the age of a fossil and its place in the series of rocks is a datum of great value. (It's another sort of comparative datum.)

Thus, the only real phylogenetic data are derived either directly or indirectly from comparison of features of specimens. You'll probably never meet a person who can show you a classification *based on* phylogeny. In a few groups, well represented in the fossil record, you may see some classifications that were *influenced* by speculations on phylogeny. Thus, this attempt to change taxonomy has not been successful.

The most recent effort to change taxonomy is the one that is least actively pressed. Strangely enough, it's the one that has the most to offer to taxonomy. This is the belief by biochemists that their data on the kinds of animals should be used by taxonomists. Much of this data is truly comparative; as such it is unquestionably of taxonomic interest.

The only difficulty is that some biochemists seem to think that all classification should be re-done on the basis of electrophoresis patterns or serological reactions. This is unrealistic. The data of biochemistry are automatically stored by taxonomy, but they are used in classification, like most other kinds of data, only when they are needed. So far, this need has been shown in very few cases, because biochemical data almost invariably confirm prior taxonomic conclusions.

Unfortunately, when the biochemical data do *not* confirm, the biochemists usually assume that their data must be wrong. For example, at a conference on biochemical taxonomy at Lawrence, Kansas, a couple of years ago, most speakers compared their biochemical results with the standard taxonomic classifications. If the results agreed, they were gratified, but if the results differed from the accepted classifications, they always assumed that their results were wrong. If the results always agree, then we don't need them. If we don't believe them when they disagree, then they're useless.

There will be few cases where taxonomists will discard the older data and switch to biochemical data, but the new data will always be interesting and sometimes of conclusive value. (Here's a case where the new data can theoretically work, but the taxonomist would rather fight than switch.)

The third idea recently "forced" into the consideration of taxonomy is called Numerical Taxonomy. This is a misnomer, because whether or not it constitutes taxonomy, it's much more than just numerical; it's statistical. It's not interested in counting the number of setae but in statistically analyzing the variation in the number of them. Numerical taxonomy has been the most active of the challenging fields, as well as the most illogical; but only a suggestion can be given here of the fallacies or the nature of the attack.

Numerical Taxonomy is one of the *new* fields of systematics. At least, its protagonists describe it as new. It has been practiced in fairly sophisticated form for more than a hundred years. The only really new thing about it is its machinery, the computers. This field has been the subject of more publications than most, summarized in the book by Sokal and Sneath, *Principles of Numerical Taxonomy*. It is curious that the publications in this field seem to ignore all criticisms, as if its internal growth made each criticism irrelevant. This would be an absurd misconception.

This was called a new field of *systematics* rather than of taxonomy, because it's not a form of taxonomy but a technique useful in several branches of the more inclusive field of systematics.

Systematics is here used as the broad term for all the fields studying the diversity of organisms, the causes of the diversity, and its history. Taxonomy, then, is the actual work of distinguishing kinds and grouping them into taxa—the work that actually occupies most of the time of the people who call themselves taxonomists.

I call it *one* of the new fields because it's listed as one of several "new methods" in taxonomy. Such as: numerical methods, comparative serology, chromatography, electrophoresis, infrared spectroscopy, and cytotaxonomy; and a miscellaneous group including: chemistry, electron microscope cytology, behavior, ecology, histology, and parasitology.

Leaving aside for the moment the first of these, all the rest *produce* data about the organisms, data which are at least potentially comparative. As such, these data are automatically taxonomic. They can be recorded in the taxonomic system, and they can be directly employed in that system if there's need to do so.

The newer forms of data offered to taxonomy by these fields can be

entirely valid taxonomic data of as much value as any older forms of data. But it's a mistake to expect to have them *used* widely. This is simply because we have already accomplished the erection of an elaborate system using the older data. We can't now switch to the newer forms, discarding much of the older work, unless there are real advantages. There usually are none, because the really new conclusions from the new data, on the rare occasions when they are different, can be integrated into the old system without starting all over again.

Even so, the verification and adjustment of the older conclusions are valuable and desirable. It's part of the normal process of growth of taxonomy.

On the other hand, the first item on this list, Numerical Taxonomy, doesn't claim to produce new data. It *analyzes* the old and new data alike. This is fine. Much can be gained by such analysis of variation. But the numericists go much farther and claim that they are *doing* taxonomy, that the machines produce classifications. In the sense that a taxonomist is likely to understand this, the claim is completely false.

In order to justify the statistical and computer work which they claim is taxonomy, the numericists make a bitter attack on the classical methods of taxonomy. Unfortunately, they prove to be so ignorant of what taxonomy is that their charges against taxonomy are ridiculous. Numerical writers admit that "numerical taxonomy would have no claim to the serious attention of biologists unless it could overcome some of the faults found in conventional taxonomic procedure."

This seems to be fair enough. But the faults which are then cited are a curious lot. The general critical conclusions of Sokal and Sneath give some idea of the quality of this attack. They say that taxonomy is a neglected discipline which has made little progress in this century (or longer), is unstable in its results, is inadequate in theory and practice, and is subject to many ills such as unreliability, failure to recruit high caliber students, circular reasoning, and the admission of work done by amateurs. It's said that "little work has been directed toward the conceptual basis of classification and indeed, the taxonomy of today is but little advanced from that of a hundred or even two hundred years ago."

If these things are true, then there is indeed much room for numericists or someone to lead us into improved methods and results. But are they true? Here is the curious thing: several of these charges are completely true; what is false is the implication that it would be better if it were not so. The last criticism cited, for example, about there being no change in procedures for two hundred years. This is true. The implication that this is a bad situation is entirely false. The methods and logic of classifica-

tion, as developed by the ancient philosophers and adopted by Linnaeus and his followers, works as well today as it did 200 years ago. Taxonomists have had very little reason to want to change it or even to discuss it.

The fact is that the numericists are so far from understanding the nature of taxonomy that their criticisms are simply irrelevant, and their claims of replacing it with something better are meaningless.

This doesn't mean that there is nothing of value to taxonomy in statistical methods. It simply means that statistics offers taxonomy valuable methods of analysis of variation and related things, but does *not*, because it *cannot*, produce taxonomic data or classifications.

It seems to me to be the critical answer to all the sensible criticisms that taxonomic results, which are in the nature of hypotheses, must be testable, and, if the later worker finds them inadequate, that he be able to emend them, to correct them. This is the basis of conventional taxonomy; it's not an obvious feature of numerical taxonomy.

The work of a taxonomist consists of three things, besides the routine matters of collecting, curating, and describing species: First, the selection of characters to be used for discrimination; second, the comparative analysis of the characters in the specimens, to find out if they're variable, and so on; and third, the assignment of the resulting groups to levels in the taxonomic hierarchy, deciding whether the group is a subfamily or a distinct family, for example. Numerical studies are able to help us with the second; they have no usefulness in the first or third.

You'll find certain expressions common in the taxonomic literature of our times. The oldest is The New Systematics. Also biosystematics, biospecies, biological species concept, natural classification, and others. These are supposed to reflect modern approaches or new developments in taxonomy. If you will examine them carefully you'll find that they are in an odd position: They are useless without the conventional taxonomy as a starting point. Furthermore, they have no actual workable basis other than the comparative data of the conventional taxonomy. They may be useful in theoretical discussions, but they're almost useless in taxonomic work.

It is well to reiterate what is meant by the expression *modern conventional taxonomy*. All successful zoological and botanical taxonomy is based on selected comparative data drawn from individual organisms. The primary feature of this system is the use of all available data of whatever sort, *so far as necessary*. By "available data" is meant comparative data of any particular sort that is available for all the objects or taxa

being classified. We can't classify unless we have this particular data for all the included items.

For instance, if you have ten species of insects among which blood analysis gave two clear-cut groups except for one species in which the individuals were so small that they had too little blood for analysis, you couldn't use this distinction in your classification of the ten species. Or, if you had records of the distinctive food habits of all but one, you could use this datum only as supporting evidence, not as basis for the classification.

A further qualification was that we use all available data *so far as necessary*. This means that when a satisfactory classification is produced we stop looking for other data. We use the most available data first and go on to use other data only when the obvious ones fail to give an effective scheme. So we would use biochemical data, for example, only when external structure is inadequate.

By data, we mean, of course, anything that can be known about the organisms, whether it's morphological, biochemical, reproductive, or behavioral. Anything that can be compared from one kind to another.

In this system, the extensive background of the taxonomist enables him to pass over, almost without conscious thought, all the non-varying features of the organisms, as well as the ones due to sex, age, pathology, and so on, and to use a workable number of features that are evidently correlated with many unmentioned ones. All features of the organisms are considered, so far as they are available, but only those are employed which are necessary to show the groupings and distinctions that occur.

When we find cases in which developmental patterns, or behavioral patterns, or biochemical components, are not correlated with more readily observed features, then will be the time to use these less obvious features in the classification. There have already been cases of this. They're exceptional and apparently rare. In the ordinary situation, use of the visible and usually structural features involves many unseen but directly correlated other features, so that even a "morphological" system is in reality not exclusively based on one type of feature.

This conventional system, then, is an all-seeing or all-considering system. It does not pretend to use all features, because it decides against the use of some. It knows of the probable existence of other features which it doesn't have access to. It stores all these data, whether or not it uses them.

This has been called the omnispective system. It has classified a million animals and more than a third of a million plants, so effectively that

every little failure irks us and leads some of us to say that the system is inadequate. It's merely not yet complete.

It's based entirely on comparative data, the only thing yet discovered on which it could be based. We still need taxonomists of varied interests to continue the work of assembling these data, and especially for the work of classifying—translating the comparative data into groups which we call taxa, so that we can come closer to complete knowledge of the apparently unlimited diversity of the living world.

Records and Descriptions of Mexican and Central American Tillomorphini

(Coleoptera: Cerambycidae)

JOHN A. CHEMSAK
University of California, Berkeley

The tribe Tillomorphini is comprised of a rather homogenous group of species in the Nearctic and Neotropical regions. Apparently this group is closely related to the Anaglyptini with one of the major differences between the tribes being the presence of eburneous elytral fasciae in the Tillomorphini. Linsley (1964) considered *Tilloclytus* Bates, *Cyrtophorus* LeConte, and *Microclytus* LeConte as anaglyptine while *Euderces* LeConte, *Tetranodus* Schaeffer, and *Pentanodes* Schaeffer were placed in the Tillomorphini. Also at this time Linsley synonymized *Eplophorus* Chevrolat with *Euderces*. It becomes obvious after examining a relatively large amount of material that this synonymy is justified. The characters of the antennal spines, palpal apices, and basal elytral gibbosities vary greatly in the available species. However, for purposes of convenience, both generic names will be utilized here. While no attempt is made at this time to critically analyze the tribal relationships of these groups, the following New World genera may be considered as tillomorphine: *Euderces, Eplophorus, Cleozona* Bates, *Tetranodus, Pentanodes, Tillomorpha* Blanchard, *Lamproclytus* Fisher, and *Calliclytus* Fisher. The other genera listed in Blackwelder (1946) are probably Anaglyptini or other.

Most Tillomorphini are rare in collections although the adults may be collected on flowers. Four genera are known from Mexico and Central America while the remainder are South American and West Indian.